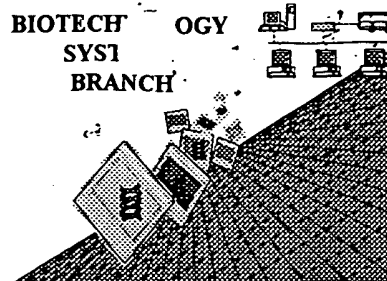


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/889,317  
Source: P4/09  
Date Processed by STIC: 7/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/889,317

DATE: 07/27/2001

TIME: 19:16:01

Input Set : A:\Tripp et al seq list.txt

Output Set: N:\CRF3\07272001\I889317.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE  
5 SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS FOR  
6 DISEASE CONTROL  
7 RALPH A. TRIPP  
8 LARRY J. ANDERSON  
9 DEBORAH D. MOORE  
11 <120> TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT  
12 OF DISEASES CAUSED BY AN INFLAMMATORY RESPONSE  
15 <130> FILE REFERENCE: 66777 / PCT  
17 <140> CURRENT APPLICATION NUMBER: US/09/889,317  
18 <141> CURRENT FILING DATE: 2001-07-13  
20 <150> PRIOR APPLICATION NUMBER: 60/116,835  
21 <151> PRIOR FILING DATE: 1999-01-22  
23 <160> NUMBER OF SEQ ID NOS: 2  
25 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 13  
29 <212> TYPE: PRT  
30 <213> ORGANISM: UNKNOWN OK  
32 <220> FEATURE:  
33 <223> OTHER INFORMATION: neuropeptide  
35 <400> SEQUENCE: 1  
36 Met Leu Gly Phe Phe Gln Gln Pro Lys Pro Lys Pro Arg  
37 1 5 10  
39 <210> SEQ ID NO: 2  
40 <211> LENGTH: 5  
41 <212> TYPE: PRT  
42 <213> ORGANISM: UNKNOWN see item 11 on Eva summary sheet  
44 <220> FEATURE:  
45 <221> NAME/KEY: UNSURE  
46 <222> LOCATION: (2)...(2)  
47 <223> OTHER INFORMATION: Xaa = any amino acid  
49 <400> SEQUENCE: 2  
50 Phe Xaa Gly Leu Met  
51 1 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/889,317

DATE: 07/27/2001

TIME: 19:16:02

Input Set : A:\Tripp et al seq list.txt

Output Set: N:\CRF3\07272001\I889317.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/889,317
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) <u>2</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	